

Global Pattern Recognition v3.4

A p-value = 0.05 82 Genes				B p-value = 0.05 82 Genes				C p-value = 0.05 82 Genes			
Cycle Cutoff = 37.5 74 Normalizers				Cycle Cutoff = 37.5 74 Normalizers				Cycle Cutoff = 37.5 82 Normalizers			
Gene	# Hits	Score	Fold vs TBP	Gene	# Hits	Score	Fold vs TBP	Gene	# Hits	Score	Fold vs TBP
Scya20	66	0.892	24.6	Scya20	62	0.838	18.4	IL-12 p35	23	0.280	2.3
IL1b	62	0.838	6.8	IL1b	59	0.797	6.0	B2m	13	0.159	1.6
Tnfrsf17	53	0.716	7.1	B2m	52	0.703	3.5	Cxcr1	13	0.159	-1.7
Cd5	44	0.595	-2.4	Il10	52	0.703	4.5	CD3e	8	0.098	-1.4
IL10	40	0.541	3.1	Terz	51	0.689	-3.9	Fcgr1	8	0.098	-1.6
Cor8	37	0.500	-2.3	Tnfrsf17	50	0.676	6.4	MIG	8	0.098	1.9
Prdm1	35	0.473	2.6	Fcgr1	37	0.5	2.0	Scya3	5	0.061	-1.3
Scya3	35	0.473	1.9	Cor8	35	0.473	-2.6	Tlr4	5	0.061	-1.5
Fcgr1	34	0.459	1.9	Prdm1	34	0.459	2.9	B-Actin	4	0.049	-1.5
B2m	29	0.392	2.2	Cd5	34	0.459	-2.2	Bad	4	0.049	1.3
Cmkbr7.2	29	0.392	-1.7	Cxcr1	32	0.432	-2.1	Cd80	4	0.049	-1.3
BAFF	28	0.378	2.0	Fcer1g	32	0.432	3.0	ICAM2	4	0.049	1.2
SLC	28	0.378	-2.4	Fcgr3	31	0.419	1.6	Interferon gamma	4	0.049	-1.5
FLIP(L)	26	0.351	-1.7	Scya3	30	0.405	1.4	Terz	4	0.049	-2.2
Cd34	25	0.338	-1.6	Fas	29	0.392	1.5	Cmkbr7.2	3	0.037	1.2
Sell	25	0.338	-1.5	IL-18	29	0.392	1.7	CTLA4	3	0.037	-1.5
Bid	22	0.297	1.8	Cyclophilin	28	0.378	1.5	Sell	3	0.037	1.1
Ilmgr2	22	0.297	1.4	FLIP(L)	28	0.378	-1.7	Scya19	3	0.037	-1.3
Fcgr3	22	0.297	1.5	Ilmgr2	28	0.378	1.5	Tgfb1	3	0.037	1.1
IL7	21	0.284	-1.4	Integrin ax	28	0.378	2.0	Tlr9	3	0.037	-1.1
Itgal	21	0.284	-1.7	B-Actin	27	0.365	-1.9	Trance	3	0.037	-1.3
Cd4	18	0.243	-1.6	STAT1	27	0.365	1.7	Cyclophilin	2	0.024	1.3
STAT1	17	0.230	1.6	Itgal	26	0.351	-2.0	BAFFR	2	0.024	-1.1
TranceLigand	17	0.230	1.5	Bad	25	0.338	1.6	Bid	2	0.024	-1.3
Cmkbr2.1	16	0.216	1.4	P-Selectin	24	0.324	1.3	Cmkbr2.1	2	0.024	-1.1
Cd8b	15	0.203	-2.2	Cmkbr2.1	23	0.311	1.3	CCR9	2	0.024	1.1
Myd88	15	0.203	-1.1	CD3e	23	0.311	-1.9	I-TAC	2	0.024	-2.9
Fcer1g	14	0.189	1.7	I-TAC	22	0.297	-2.9	FasL	2	0.024	-1.7
GPI	13	0.176	-1.2	Fcgr1	22	0.297	-2.0	FLIP(L)	2	0.024	-1.0
Bad	13	0.176	1.2	GPI	21	0.284	-1.2	IL2rg	2	0.024	1.0
CD28	13	0.176	1.1	Blr1	21	0.284	1.0	Itgal	2	0.024	-1.1
Integrin ax	13	0.176	1.7	Cmkbr7.2	21	0.284	-1.5	Fcgr3	2	0.024	1.1
Fas	12	0.162	1.3	Cd4	21	0.284	-2.0	Tlr2	2	0.024	1.2
Fcer1a	12	0.162	-2.3	Sell	21	0.284	-1.4	Blr1	1	0.012	-1.1
P-Selectin	12	0.162	1.3	Hprt	20	0.27	1.2	CXCR3.1	1	0.012	1.4
Tlr2	12	0.162	1.1	Cd80	20	0.27	-1.3	CD28	1	0.012	-1.3
Cyclophilin	11	0.149	1.2	IL-12 p35	20	0.27	2.0	Cd34	1	0.012	1.2
Hprt	11	0.149	1.2	TBP	20	0.27	1.0	Cd4	1	0.012	-1.3
Cd86	11	0.149	-1.1	Cd34	19	0.257	-1.3	Cd86	1	0.012	-1.1
VEGF	11	0.149	-1.1	ICAM1.2	19	0.257	-1.5	Fas	1	0.012	1.2
TBP	11	0.149	1.0	Tlr4	19	0.257	-1.7	Fcer1g	1	0.012	1.8
Blr1	10	0.135	1.1	Bid	18	0.243	1.4	ICAM1.2	1	0.012	-1.0
Tlr4	10	0.135	-1.1	Cd44	18	0.243	1.2	IL10	1	0.012	1.4
Tlr9	10	0.135	-1.0	IL2rg	18	0.243	-1.1	IL1b	1	0.012	-1.1
Tnf	10	0.135	1.0	Tnfrsf1b	18	0.243	-1.4	Myd88	1	0.012	-1.1
Trance	10	0.135	1.1	VEGF	18	0.243	-1.3	Nos2	1	0.012	-1.9
CD3e	9	0.122	-1.4	Cd8b	17	0.23	-1.7	RANTES	1	0.012	1.3
IL15	9	0.122	-1.2	Myd88	16	0.216	-1.1	SLC	1	0.012	1.4
IL2rg	9	0.122	-1.1	SLC	16	0.216	-1.7	STAT1	1	0.012	1.1
Jag-1	8	0.108	-1.5	Cd86	15	0.203	-1.2	Tnf	1	0.012	-1.3
ICAM1.2	8	0.108	-1.2	Tlr9	15	0.203	-1.1	TranceLigand	1	0.012	-1.2
ICAM2	8	0.108	-1.1	Trance	15	0.203	-1.1	VEGF	1	0.012	-1.1
IL-12 p35	8	0.108	-1.1	IL7	14	0.189	-1.5	TBP	1	0.012	1.0
CCXCR1.1	7	0.095	-1.2	CD28	13	0.176	-1.1	GPI	0	0.000	-1.0
B-Actin	6	0.081	-1.3	IL4	13	0.176	1.7	Hprt	0	0.000	1.1
BAFFR	6	0.081	-1.0	Tlr2	13	0.176	1.3	18s rRNA	0	0.000	-1.7
Cd80	6	0.081	-1.0	TranceLigand	13	0.176	1.2	Art2b	0	0.000	-1.1
Interferon gamma	6	0.081	2.4	CTLA4	12	0.162	-1.7	BAFF	0	0.000	-1.6
Tnfrsf1a	6	0.081	1.0	Tnfrsf1a	12	0.162	1.0	Bcl-6	0	0.000	-1.0
Bcl-6	5	0.068	1.0	Tgfb1	11	0.149	1.1	BCMA	0	0.000	-1.1
Fcgr1	5	0.068	-1.2	BAFFR	10	0.135	-1.2	BLIMP	0	0.000	1.1
Terz	5	0.068	-1.8	Bcl-6	10	0.135	-1	Cmkar4.1	0	0.000	-1.3
Tgfb1	5	0.068	-1.0	Lymphotactin	10	0.135	1.2	CCR8	0	0.000	-1.1
Nos2	4	0.054	-1.0	Itgam	9	0.122	-1.2	Cd44	0	0.000	2.2
RANTES	4	0.054	-1.1	Scya19	9	0.122	-1.4	Cd5	0	0.000	1.1
Scya19	4	0.054	-1.0	ICAM2	7	0.095	-1.0	Cd8b	0	0.000	1.2
CTLA4	3	0.041	-1.1	FasL	6	0.081	-1.5	Fcer1a	0	0.000	1.3
Lymphotactin	3	0.041	1.2	RANTES	6	0.081	1.1	Ilmgr2	0	0.000	1.0
FasL	2	0.027	1.1	Tnf	6	0.081	-1.3	IL15	0	0.000	1.4
CXCR3.1	1	0.014	1.1	Fcer1a	5	0.068	-1.8	IL-18	0	0.000	3.2
Cmkar4.1	1	0.014	1.4	CXCR3.1	4	0.054	1.4	IL4	0	0.000	1.1
CCR9	1	0.014	1.3	Jag-1	4	0.054	-1.3	IL6	0	0.000	-1.5
Cd44	1	0.014	-1.8	Nos2	4	0.054	-1.9	IL7	0	0.000	-1.0
IL4	1	0.014	1.6	Art2b	3	0.041	1.0	Fcgr1	0	0.000	1.1
18s rRNA	0	0.000	1.4	Cmkar4.1	2	0.027	1.1	Integrin ax	0	0.000	1.2
Art2b	0	0.000	1.2	IL15	2	0.027	1.2	Itgam	0	0.000	-1.1
I-TAC	0	0.000	-1.0	Interferon gamma	2	0.027	1.6	Jag-1	0	0.000	1.1
IL-18	0	0.000	-1.9	CCR9	1	0.014	1.4	Lymphotactin	0	0.000	-1.0
IL6	0	0.000	2.0	18s rRNA	0	0	-1.2	P-Selectin	0	0.000	1.0
Itgam	0	0.000	-1.1	BAFF	0	0	1.3	Scya20	0	0.000	-1.3
MIG	0	0.000	-2.6	IL6	0	0	1.3	Tnfrsf1a	0	0.000	-1.0
Tnfrsf1b	0	0.000	-6.4	MIG	0	0	-1.3	Tnfrsf1b	0	0.000	4.5
CCR5	-1	N.S.	1.1	CCR5	-1	N.S.	1.6	CCR5	-1	N.S.	1.4
CD38	-1	N.S.	-3.1	CD38	-1	N.S.	-2.2	CD38	-1	N.S.	1.4
CmkbrIL2.1	-1	N.S.	-3.5	CmkbrIL2.1	-1	N.S.	-3.1	CmkbrIL2.1	-1	N.S.	1.1
Csf1	-1	N.S.	-2.3	Csf1	-1	N.S.	-2.6	Csf1	-1	N.S.	-1.1
Csf3	-1	N.S.	-2.2	Csf3	-1	N.S.	-2.9	Csf3	-1	N.S.	-1.3
Ilfb	-1	N.S.	1.7	Ilfb	-1	N.S.	-1.1	Ilfb	-1	N.S.	-1.9
IL12rb2	-1	N.S.	1.4	IL12rb2	-1	N.S.	1.1	IL12rb2	-1	N.S.	-1.3
Il1r1	-1	N.S.	-3.5	Il1r1	-1	N.S.	-3.1	Il1r1	-1	N.S.	1.1
Il1rak	-1	N.S.	1.2	Il1rak	-1	N.S.	-1.7	Il1rak	-1	N.S.	-2.0
IL2	-1	N.S.	-1.6	IL2	-1	N.S.	-2.3	IL2	-1	N.S.	-1.4
IL2ra	-1	N.S.	-3.4	IL2ra	-1	N.S.	-1.5	IL2ra	-1	N.S.	2.3
Interferon alpha 1	-1	N.S.	1.0	Interferon alpha 1	-1	N.S.	-2.3	Interferon alpha 1	-1	N.S.	-2.4
Scyd1	-1	N.S.	-3.5	Scyd1	-1	N.S.	-3.1	Scyd1	-1	N.S.	1.1
SOCS-1	-1	N.S.	1.6	SOCS-1	-1	N.S.	1.2	SOCS-1	-1	N.S.	-1.3

Supplemental Figure S1

Quantitative gene expression analysis of K/BxN popliteal LNs. The cDNA from popliteal LNs from 15- to 16-week-old five sick *FcRn*^{+/+}, five sick *FcRn*^{-/-}, and five healthy *FcRn*^{-/-} mice was prepared and analyzed individually for expression of the genes indicated. Comparison of five healthy *FcRn*^{-/-} mice with (A) five sick *FcRn*^{+/+} mice and (B) five sick *FcRn*^{-/-} mice show a similar pattern of gene expression changes. (C) No significant expression changes were detected when five sick *FcRn*^{+/+} and five sick *FcRn*^{-/-} mice were compared. Of 96 ImmunoQuantArray genes analyzed, 82 were expressed with *C_t* values below a 37.5 cycle cutoff, and thus were eligible for GPR analysis. The number of genes qualifying as normalizers (because they showed no significant expression changes) is indicated. # Hits (and the fractional GPR score) indicates the number (and fraction) of normalizer genes that suggested that there was a significant ($P \leq 0.05$) expression change of the test gene in the experimental cohort comparison. GPR scores greater than or equal to 0.4 are considered highly reliable. Fold changes, up (red) or down (green), are based on normalization to TATA box-binding protein (TBP).